WHAT IS CLAIMED IS:

1. A method of detecting one or more polypeptides in a sample, the method comprising:

a) contacting the sample with at least one genetic package that displays a polypeptide-binding component, wherein:

the genetic package comprises a predetermined marker component; and

the polypeptide binding component specifically binds to at least one of the polypeptides;

b) amplifying the genetic package, resulting in an amplified genetic package, or amplifying the marker component in the genetic package;

c) detecting the marker component, wherein the presence of the marker component indicates the presence of the one or more polypeptides.

2. The method of claim 1, wherein the one or more polypeptides comprise one or more protein, biotinylated protein, isolated protein, recombinant protein, enzyme, enzyme substrate, cancer protein, or disease related protein.

3. The method of claim 1, wherein the one or more polypeptides in the sample or the at least one genetic package is bound to a solid support.

4. The method of claim 3, wherein the solid support comprises one or more of a microsphere or bead, a surface of a tube or plate or a filter membrane.

5. The method of claim 3, further comprising washing the solid support after the polypeptide binding component specifically binds at least one of the one or more polypeptides.

6. The method of claim 1, comprising concurrently detecting at least about 10 to about 10^9 polypeptides.

7. The method of claim 6, comprising concurrently detecting at least about 50 to about 10,000 polypeptides.

8. The method of claim 6, comprising concurrently detecting at least about 3 to about 500 polypeptides.

9. The method of claim 6, comprising concurrently detecting at least about 3 to about 100 polypeptides.

10. The method of claim 1, wherein the sample is a tissue sample, a blood sample, a cell lysate or a plurality of cultured cells.

11. The method of claim 1, wherein the genetic package comprises a bacteriophage, a baculovirus or a bacterium.

12. The method of claim 11, wherein the bacteriophage comprises T4 phage, M13 phage or λ phage.

13. The method of claim 1, wherein step (a) comprises contacting the sample with a plurality of bio-displayed polypeptide binding components.

14. The method of claim 13, wherein the plurality of bio-displayed polypeptide binding components comprises about 10^2 to about 10^{10} different polypeptide-binding components.

15. The method of claim 13, wherein the plurality of bio-displayed polypeptide binding components comprises about 10^5 to about 10^{10} different polypeptide-binding components.

16. The method of claim 13, wherein each member of the plurality of bio-displayed polypeptide-binding components is associated with a different marker component, resulting in a plurality of marker components.

17. The method of claim 16, wherein the plurality of marker components comprises a plurality of related marker components.

18. The method of claim 1, wherein the polypeptide-binding component comprises one or more of an agent selected from among an antibody, an antibody fragment, a single chain antibody fragment, an enzyme, biotin, avidin, streptavidin, a ligand and a receptor.

19. The method of claim 18, wherein the antibody, the antibody fragment or the single chain antibody fragment comprises one or more antigen recognition regions.

20. The method of claim 1, wherein step (c) comprises detecting the marker component by a method selected from among mass spectrometry, NMR spectroscopy, hybridization, microarray detection, electrophoretic detection, surface plasmon resonance, electrochemical detection, fluorescent detection, chemiluminescent detection, colorimetric detection and electrochemiluminescent detection.

21. The method of claim 20, wherein mass spectrometry comprises matrix-assisted laser desorption/ionization (MALDI) time-of-flight (TOF) mass spectrometry.

22. The method of claim 1, further comprising determining an amount of the marker component.

23. The method of claim 22, comprising correlating the amount of the marker component to an amount of at least one of the one or more polypeptides in the sample.

24. The method of claim 1, wherein the predetermined marker comprises one or more signature polypeptides.

25. The method of claim 23, wherein at least one of the one or more signature polypeptide is derived from hemoglobin.

26. The method of claim 1, wherein the genetic package comprises a surface and wherein the marker component comprises a nucleic acid, which nucleic acid encodes a polypeptide, which polypeptide is expressed on the surface of the genetic package.

27. The method of claim 1, the predetermined marker comprises a nucleic acid fragment.

28. The method of claim 27, wherein amplifying the marker component comprises performing polymerase chain reaction, ligase chain reaction, or Qβ-replicase amplification of the nucleic acid fragment or a detectable portion thereof.

29. An integrated system for detecting one or more polypeptide in one or more sample, the system comprising:

a) a solid support comprising the one or more polypeptide;

b) a plurality of bio-displayed polypeptide binding components that bind to one or more of the one or more polypeptides, and are each associated with a different marker component;

c) an assay module for amplifying or expressing the marker component;

d) a detection module for receiving the marker component or a derivative thereof, wherein the detection system detects one or more different marker component and determines an amount of the one or more different marker component; and,

e) an analyzing module in operational communication with the detection system that comprises a computer or computer readable medium comprising one or more instruction set for correlating the amount of the one or more different marker component with the one or more polypeptide.

30. The system of claim 29, wherein the assay module, during operation, is operably coupled to the solid support and the detection system.

31. The system of claim 29, wherein the detection module comprises a mass spectrometer, an NMR spectrometer, an optical detector, or a fluorescent detector.

32. The system of claim 31, wherein the mass spectrometer, during operation, is operably coupled to solid support and to the assay system.

33. The system of claim 29, wherein the analyzing module calculates a ratio of at least a first marker component to at least a second marker component.

34. The system of 29, wherein the analyzing module correlates the ratio to a ratio of at least a first polypeptide to at least a second polypeptide in the one or more sample.

35. The system of claim 29, wherein the detection module generates a plurality of data points based upon the amount of each marker component.

36. The system of claim 35, wherein the computer or computer readable medium comprises an instruction set for organizing the data points into a database that comprises a profile for the one or more sample.

37. The system of claim 36, wherein the profile for the one or more sample identifies an expression level of at least one of the one or more polypeptide in the sample and a functional state of at least one of the one or more polypeptide in the sample.

38. The system of claim 29, wherein the one or more instruction set comprises software for generating a graphical representation of the amount of the one or more polypeptides.

39. The system of claim 35, wherein the one or more instruction set comprises software for performing multivariate analysis for the plurality of data points.

40. The system of claim 35, wherein the one or more instruction set comprises software for performing principle component analysis or difference analysis upon the plurality of data points.

41. The system of claim 29, further comprising an output file embodied in a computer readable medium.

42. The output file produced by the system of claim 41.

43. A combination, comprising:

a library of phage with a phage displayed binding protein, and a sequence of nucleotides encoding a signature protein in the genome; and

a list denoting the protein displayed on each phage and corresponding signature protein.

44. The combination of claim 43, wherein the list is a database.

45. The combination of claim 43, wherein the list is stored in a computer or on a computer-readable medium.

46. The method of claim 1, wherein the sample comprises a plurality of polypeptides that each bind to different polypeptide-binding component.

47. The method of claim 3, wherein the solid support comprises a microtiter dish or well, a glass slide, a silicon chip, a nitrocellulose sheet or nylon mesh.

48. The method of claim 1, wherein the sample comprises a tissue sample, a body fluid, an organ or cultured cells.